

SEQUENCE LISTING

<110> Welcher, Andrew A.  
Calzone, Frank J.

<120> CD20/IgE-Receptor Like Molecules and Uses Thereof

<130> 01017/36938A

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<150> US 09/723,258

<151> 2000-11-27

<150> US 60/193,728

<151> 2000-03-30

<160> 25

<170> PatentIn Ver. 2.0

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<222> (98)..(697)

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Met Asp Ser Ser Thr Ala  
1 5

cac agt ccg gtg ttt ctg gta ttt cct cca gaa atc act gct tca gaa 163  
His Ser Pro Val Phe Leu Val Phe Pro Pro Glu Ile Thr Ala Ser Glu  
10 15 20

tat gag tcc aca gaa ctt tca gcc acg acc ttt tca act caa agc ccc 211  
Tyr Glu Ser Thr Glu Leu Ser Ala Thr Thr Phe Ser Thr Gln Ser Pro  
25 30 35

ttg caa aaa tta ttt gct aga aaa atg aaa atc tta ggg act atc cag 259  
Leu Gln Lys Leu Phe Ala Arg Lys Met Lys Ile Leu Gly Thr Ile Gln  
40 45 50

atc ctg ttt gga att atg acc ttt tct ttt gga gtt atc ttc ctt ttc 307  
Ile Leu Phe Gly Ile Met Thr Phe Ser Phe Gly Val Ile Phe Leu Phe  
55 60 65 70

act ttg tta aaa cca tat cca agg ttt ccc ttt ata ttt ctt tca gga 355  
Thr Leu Leu Lys Pro Tyr Pro Arg Phe Pro Phe Ile Phe Leu Ser Gly  
75 80 85

tat cca ttc tgg ggc tct gtt ttg ttc att aat tct gga gcc ttc cta 403  
Tyr Pro Phe Trp Gly Ser Val Leu Phe Ile Asn Ser Gly Ala Phe Leu  
90 95 100

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att gca gtg aaa aga aaa acc aca gaa act ctg ata ata ttg agc cga 451
Ile Ala Val Lys Arg Lys Thr Thr Glu Thr Leu Ile Ile Leu Ser Arg
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ata atg aat ttt ctt agt gcc ctg gga gca ata gct gga atc att ctc 499
Ile Met Asn Phe Leu Ser Ala Leu Gly Ala Ile Ala Gly Ile Ile Leu
      120                      125                      130

ctc aca ttt ggt ttc atc cta gat caa aac tac att tgt ggt tat tct 547
Leu Thr Phe Gly Phe Ile Leu Asp Gln Asn Tyr Ile Cys Gly Tyr Ser
      135                      140                      145                      150

cac caa aat agt cag tgt aag gct gtt act gtc ctg ttc ttg gga att 595
His Gln Asn Ser Gln Cys Lys Ala Val Thr Val Leu Phe Leu Gly Ile
      155                      160                      165

ttg att aca ttg atg act ttc agc att att gaa tta ttc att tct ctg 643
Leu Ile Thr Leu Met Thr Phe Ser Ile Ile Glu Leu Phe Ile Ser Leu
      170                      175                      180

cct ttc tca att ttg ggg tgc cac tca gag gat tgt gat tgt gaa caa 691
Pro Phe Ser Ile Leu Gly Cys His Ser Glu Asp Cys Asp Cys Glu Gln
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Cys Cys
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aaaaaaaaaaaa aaa 760

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Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg Lys Met Lys
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Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr Phe Ser Phe
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Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro Arg Phe Pro
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Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val Leu Phe Ile
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Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr Thr Glu Thr
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Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala Leu Gly Ala
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Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu Asp Gln Asn
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Tyr	Ile	Cys	Gly	Tyr	Ser	His	Gln	Asn	Ser	Gln	Cys	Lys	Ala	Val	Thr
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Val	Leu	Phe	Leu	Gly	Ile	Leu	Ile	Thr	Leu	Met	Thr	Phe	Ser	Ile	Ile
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Met Leu Leu															1
caa tcc caa acc atg ggg gtt tct cac agc ttt aca cca aag ggc atc															163
Gln Ser Gln Thr Met Gly Val Ser His Ser Phe Thr Pro Lys Gly Ile															5 10 15
act atc cct caa aga gag aaa cct gga cac atg tac caa aac gaa gat															211
Thr Ile Pro Gln Arg Glu Lys Pro Gly His Met Tyr Gln Asn Glu Asp															20 25 30 35
tac ctg cag aac ggg ctg cca aca gaa acc acc gtt ctt ggg act gtc															259
Tyr Leu Gln Asn Gly Leu Pro Thr Glu Thr Thr Val Leu Gly Thr Val															40 45 50
cag atc ctg tgt tgc ctg ttg att tca agt ctg ggg gcc atc ttg gtt															307
Gln Ile Leu Cys Cys Leu Leu Ile Ser Ser Leu Gly Ala Ile Leu Val															55 60 65
ttt gct ccc tac ccc tcc cac ttc aat cca gca att tcc acc act ttg															355
Phe Ala Pro Tyr Pro Ser His Phe Asn Pro Ala Ile Ser Thr Thr Leu															70 75 80
atg tct ggg tac cca ttt tta gga gct ctg tgt ttt ggc att act gga															403
Met Ser Gly Tyr Pro Phe Leu Gly Ala Leu Cys Phe Gly Ile Thr Gly															85 90 95
tcc ctc tca att atc tct gga aaa caa tca act aag ccc ttt gac ctg															451
Ser Leu Ser Ile Ile Ser Gly Lys Gln Ser Thr Lys Pro Phe Asp Leu															100 105 110 115
agc agc ttg acc tca aat gca gtg agt tct gtt act gca gga gca ggc															499
Ser Ser Leu Thr Ser Asn Ala Val Ser Ser Val Thr Ala Gly Ala Gly															120 125 130

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ctc ttc ctc ctt gct gac agc atg gta gcc ctg agg act gcc tct caa 547
Leu Phe Leu Leu Ala Asp Ser Met Val Ala Leu Arg Thr Ala Ser Gln
135 140 145

cat tgt ggc tca gaa atg gat tat cta tcc tca ttg cct tat tcg gag 595
His Cys Gly Ser Glu Met Asp Tyr Leu Ser Ser Leu Pro Tyr Ser Glu
150 155 160

tac tat tat cca ata tat gaa atc aaa gat tgt ctc ctg acc agt gtc 643
Tyr Tyr Tyr Pro Ile Tyr Glu Ile Lys Asp Cys Leu Leu Thr Ser Val
165 170 175

agt tta aca ggt gtc cta gtg gtg atg ctc atc ttc act gtg ctg gag 691
Ser Leu Thr Gly Val Leu Val Val Met Leu Ile Phe Thr Val Leu Glu
180 185 190 195

ctc tta tta gct gca tac agt tct gtc ttt tgg tgg aaa cag ctc tac 739
Leu Leu Leu Ala Ala Tyr Ser Ser Val Phe Trp Trp Lys Gln Leu Tyr
200 205 210

tcc aac aac cct ggg agt tca ttt tcc tcg acc cag tca caa gat cat 787
Ser Asn Asn Pro Gly Ser Ser Phe Ser Ser Thr Gln Ser Gln Asp His
215 220 225

atc caa cag gtc aaa aag agt tct tca cgg tct tgg ata taagtaactc 836
Ile Gln Gln Val Lys Lys Ser Ser Ser Arg Ser Trp Ile
230 235 240

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35 40 45

Gly Thr Val Gln Ile Leu Cys Cys Leu Leu Ile Ser Ser Leu Gly Ala
50 55 60

Ile Leu Val Phe Ala Pro Tyr Pro Ser His Phe Asn Pro Ala Ile Ser
65 70 75 80

Thr Thr Leu Met Ser Gly Tyr Pro Phe Leu Gly Ala Leu Cys Phe Gly
85 90 95

Ile Thr Gly Ser Leu Ser Ile Ile Ser Gly Lys Gln Ser Thr Lys Pro
100 105 110

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Phe Asp Leu Ser Ser Leu Thr Ser Asn Ala Val Ser Ser Val Thr Ala  
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130 135 140  
Ala Ser Gln His Cys Gly Ser Glu Met Asp Tyr Leu Ser Ser Leu Pro  
145 150 155 160  
Tyr Ser Glu Tyr Tyr Tyr Pro Ile Tyr Glu Ile Lys Asp Cys Leu Leu  
165 170 175  
Thr Ser Val Ser Leu Thr Gly Val Leu Val Val Met Leu Ile Phe Thr  
180 185 190  
Val Leu Glu Leu Leu Leu Ala Ala Tyr Ser Ser Val Phe Trp Trp Lys  
195 200 205  
Gln Leu Tyr Ser Asn Asn Pro Gly Ser Ser Phe Ser Ser Thr Gln Ser  
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<210> 16  
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<210> 18  
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<210> 19  
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<220>  
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<210> 23  
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Arg Arg Arg